

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:40:42 ; Search time 20.26 Seconds

(without alignments)
475.872 Million cell updates/sec

Title: US-09-502-984B-37

Perfect score: 1284

Sequence: 1 KFESKALLIARGPELLCF.....RKNRLDEEVERLKLQYGER 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1060	82.6	508	1	EPOR_HUMAN
2	877.5	66.3	507	1	EPOR_RAT
3	869.5	67.7	507	1	EPOR_MOUSE
4	171	13.3	625	1	TPOR_MOUSE
5	146	11.4	635	1	TPOR_HUMAN
6	118	9.2	581	1	PRUR_BOVIN
7	116	9.0	831	1	PRUR_BOVIN
8	114.5	8.9	522	1	ILVR_MELGA
9	112.5	8.8	634	1	ILVR_HUMAN
10	110.5	8.6	634	1	GHR_BOVIN
11	110	8.6	831	1	PRUR_CHICK
12	108	8.4	281	1	GCN4_YEAST
13	108	8.4	581	1	PRUR_CEREL
14	107	8.3	608	1	GHR_CHICK
15	104.5	8.1	611	1	GHR_COLLI
16	104	8.1	616	1	PRUR_RABIT
17	103.5	8.1	650	1	GHR_MOUSE
18	103.5	8.1	830	1	PRUR_COLLI
19	103	8.0	638	1	GHR_COLLI
20	99.5	7.7	638	1	GHR_PIG
21	98	7.6	638	1	GHR_RABIT
22	96.5	7.5	378	1	CYRB_HUMAN
23	96	7.5	1165	1	ILVR_HUMAN
24	94	7.3	468	1	ILVR_HUMAN
25	92.5	7.2	638	1	GHR_MOUSE
26	92	7.2	2594	1	GHR_RAT
27	91	7.1	184	1	7LBS_DROVI
28	91	7.1	184	1	MPL_MPLV
29	90	7.0	485	1	PRUR_MOUSE
30	90	7.0	485	1	HXKA_YEAST
31	89	6.9	638	1	RECG_BACSU
32	88.5	6.9	511	1	GHR_MACMU
33	88	6.9	622	1	SCRB_ZYMKO
					PL6471 homo sapien

34	88	6.9	845	1	CSW_DROME	P29349 drosophila
35	87	6.8	610	1	PRUR_RAT	P05710 rattus norv
36	86.5	6.7	406	1	GSD_BACSU	O32164 bacillus su
37	85.5	6.7	805	1	SUST_SOYBN	P13708 glycine max
38	85.5	6.7	863	1	AMPN_CAUCR	P37807 caulobacter
39	85.5	6.7	920	1	PARC_SYNY3	P73077 synechocyst
40	84.5	6.6	805	1	SUSY_PHAUV	O01390 phaseolus a
41	84.5	6.6	2561	1	PSPL_BACSU	P39845 bacillus su
42	84	6.5	336	1	CDIL_MOUSE	P11609 mus musculu
43	84	6.5	400	1	GMCR_HUMAN	P15509 homo sapien
44	84	6.5	485	1	HXKB_YEAST	P04807 saccharomyc
45	84	6.5	1136	1	TIRL_BOVIN	O06805 bos taurus

ALIGNMENTS

RESULT 1

ID EPOR_HUMAN STANDARD: PRT; 508 AA.

AC P19235; 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Erythropoietin receptor precursor (EPO-R).

GN EPOR.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91372359; PubMed=1654273;

RA Ehrenman K., St John T.;

RT "The erythropoietin receptor gene: cloning and identification of multiple transcripts in an erythroid cell line OCIW1.";

RL Exp. Hematol. 19:973-977(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=90304340; PubMed=2163696;

RA Jones S.S., D'Andrea A., Haines L.L., Wong G.G.;

RT "Human erythropoietin receptor: cloning, expression, and biologic characterization.";

RL Blood 76:31-35(1990).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=placenta;

RX MEDLINE=92399733; PubMed=1668606;

RA Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N., Hankins W.D.;

RT "Cloning of the human erythropoietin receptor gene.";

RL Blood 78:2548-2556(1991).

RN [4]

RP SEQUENCE OF 1-96 FROM N.A.

RC TISSUE=placenta;

RX MEDLINE=92399734; PubMed=1668607;

RA Maouche L., Tournamille C., Hattab C., Boifa G., Cartton J.P., Chretien S.;

RT "Cloning of the gene encoding the human erythropoietin receptor.";

RL Blood 78:2557-2563(1991).

RN [5]

RP SEQUENCE OF 1-17 FROM N.A.

RX MEDLINE=92147143; PubMed=1664413;

RA Penny L.A., Forget B.G.;

RT "Genomic organization of the human erythropoietin receptor gene.";

RL Genomics 11:974-980(1991).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.

RX MEDLINE=96291992; PubMed=8662530;

RA Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S., Wrishton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.;

RT "Functional mimicry of a protein hormone by a peptide agonist: the EPO receptor complex at 2.8 A.";

RL Science 273:464-471(1996).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.
 RX MEDLINE=99023198; PubMed=9808045;
 RA Ljvnh O., Johnson D.L., Stura E.A., Farrell F.X., Barbone F.P.,
 RA You Y., Liu K.D., Goldsmith M.A., He W., Krause C.D., Pestka S.,
 RA Jolliffe L.K., Wilson I.A.;
 RT "An antagonist peptide-EPO receptor complex suggests that receptor
 RT dimerization is not sufficient for activation.";
 RL Nat. Struct. Biol. 5:993-1004(1998).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-244 IN COMPLEX WITH EPO.
 RX MEDLINE=98445092; PubMed=9774108;
 RA Syed R.S., Reid S.W., Li C., Cheelam J.C., Aoki K.H., Liu B.,
 RA Zhan H., Ossland T.D., Chirino A.J., Zhang J., Finer-Moore J.,
 RA Elliott S., Stoney K., Katz B.A., Matthews D.J., Mendoloski J.J.,
 RA Earle J., Stroud R.M.;
 RT "Efficiency of signalling through cytokine receptors depends
 RT critically on receptor orientation.";
 RL Nature 395:511-516(1998).
 CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
 CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
 CC AND DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC -----
 DR EMBL: M34986; AA52401.1; -
 DR EMBL: M60459; AA52403.1; -
 DR EMBL: S45332; AAB23271.1; -
 DR EMBL: M76595; AA52393.1; -
 DR EMBL: M77244; AA52392.1; -
 DR PIR: A43799; A43799.
 DR PIR: A49824; A49824.
 DR PIR: A53958; A53958.
 DR PDB: 1EBP; 29-JUL-97.
 DR PDB: 1EBA; 18-NOV-98.
 DR PDB: 1EER; 01-OCT-99.
 DR PDB: 1CNA; 11-AUG-99.
 DR MIM: 133171; -
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 DR Receptor: Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 508 ERYTHROPOIETIN RECEPTOR.
 FT DOMAIN 25 250 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 251 273 POTENTIAL.
 FT DOMAIN 274 508 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 148 213 FIBRONECTIN TYPE-III.
 FT DISULFID 52 62
 FT DISULFID 91 107
 FT CARBOHYD 76 76
 SQ SEQUENCE 508 AA; 55065 MW; F9F326E162E9512A CRC64; N-LINKED (GLCNAC...) (POTENTIAL).

Query Match 82.6%; Score 1060; DB 1; Length 508;
 Best Local Similarity 93.8%; Pred. No. 9.4e-85;
 Matches 198; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFSKALLAARPEELCTERLEDLVCFPEEASAGVGNGNSFQLEDEPMKICRL 60
 |||
 |||

Db 34 KFSKALLAARPEELCTERLEDLVCFWEASAGVGNGNSFQLEDEPMKICRL 93
 QY 61 HQAPTAAGAIRFWCSLPATDTSSFPVLELRITAASGAPRFRHYIHNEVLDAPYGLVA 120
 |||
 Db 94 HQAPTAAGAIRFWCSLPATDTSSFPVLELRITAASGAPRFRHYIHNEVLDAPYGLVA 153
 QY 121 RLADDSGHVIRMLPPPEIPMTSHIRELDISGNGAGSQVRELLGRTCYLSMLRGR 180
 |||
 Db 154 RLADDSGHVIRMLPPPEIPMTSHIREVDVSGNGAGSQVRELLGRTCYLSMLRGR 213
 QY 181 TRITIAVARARAPSPFGFMSAMSEPSILTT 211
 |||
 Db 214 TRITIAVARARAPSPFGFMSAMSEPSILTT 244

RESULT 2

EPOR_RAT STANDARD; PRT; 507 AA.

ID EPOR_RAT
 AC 007303;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Erythropoietin receptor precursor (Epo-R).
 GN EPOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9326574; PubMed=7684373;
 RA Masuda S., Nagao M., Takahata K., Konishi Y., Galiyas F.,
 RA Tabita T., Sasaki R.;
 RT "Functional erythropoietin receptor of the cells with neural
 RT characteristics. Comparison with receptor properties of erythroid
 RT cells.";
 RL J. Biol. Chem. 268:11208-11216(1993).
 CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
 CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
 CC AND DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC -----
 DR EMBL: D13566; BAA02761.1; -
 DR PIR: A46713; A46713.
 DR HSSP: P19235; 1EBA.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 DR Receptor: Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 507 ERYTHROPOIETIN RECEPTOR.
 FT DOMAIN 25 249 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 250 272 POTENTIAL.
 FT DOMAIN 273 507 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 147 212 FIBRONECTIN TYPE-III.
 FT DISULFID 52 62
 FT DISULFID 90 106
 FT CARBOHYD 75 75
 SQ SEQUENCE 507 AA; 55499 MW; AC79AF22D06A7312 CRC64; N-LINKED (GLCNAC...) (POTENTIAL).

```

Query Match          68.3%; Score 877.5; DB 1; Length 507;
Best Local Similarity 78.2%; Pred. No. 6.9e-69;
Matches 165; Conservative 23; Mismatches 22; Indels 1; Gaps 1;

OY 1 KESKAAIIAARGPEELICFTEERLEDVCFEEAASAGVPGNFSFQLEDEPMKICRL 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 34 KESKAAIIAARGSEELICFTEERLEDVCFWEAASAGM-FNYSFSTQLEGSRSKSL 92
OY 61 HOAPTARCAIRPWCSLPTADTSSFPVLELRLTAASGAPRFHVIHINEVLLDAPVGLYA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 93 HOAPTVRGSRWPCSLPTADTSSFPVLELQVTEAASGSPRYHRIHINEVLLDAPAGLLA 152
OY 121 RIADSGHVIWMLPPETPMTSHIRFELDISAGNAGSVORVELLEGRTCVLSNLRG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 153 RAEEGSHVILWMLPPGAPMTTHIRYEDVSAAGNAGGTORVEVLEGRTCVLSNLRG 212
OY 181 TRITTAIVARMAEPSPFGFSAMSEPVSLT 211
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 213 TRYTFAVRARMAEPSPFGFSAMSEPVSLT 243

RESULT 3
EPOK_MOUSE          STANDARD;          PRT;          507 AA.
ID  P14753; 063852;
DT  01-APR-1990 (Rel. 14, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Erythropoietin receptor precursor (EPO-R).
GN  EPOK.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_Taxid=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89195238; PubMed=2539263;
RA  D'Andrea A.D., Lodish H.F., Wong G.G.;
RT  "Expression cloning of the murine erythropoietin receptor.";
RL  Cell 57:277-285(1989).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/C; TISSUE=Liver;
RX  MEDLINE=91080149; PubMed=2175360;
RA  Kuramochi S., Ikawa Y., Todokoro K.;
RT  "Characterization of murine erythropoietin receptor genes.";
RL  J. Mol. Biol. 216:567-575(1990).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92017832; PubMed=1656233;
RA  Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;
RT  "Unregulated expression of the erythropoietin receptor gene caused by
RT  insertion of spleen focus-forming virus long terminal repeat in a
RT  murine erythroleukemia cell line.";
RL  Mol. Cell. Biol. 11:5527-5533(1991).
RN  [4]
RP  SEQUENCE OF 1-27 FROM N.A.
RX  MEDLINE=90287158; PubMed=2162479;
RA  Youssoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;
RT  "Structure and transcription of the mouse erythropoietin receptor
RT  gene.";
RL  Mol. Cell. Biol. 10:3675-3682(1990).
RN  [5]
RP  SEQUENCE OF 1-24 FROM N.A.
RX  MEDLINE=91201346; PubMed=1849897;
RA  Lacombe C., Chretien S., Lemarchandel V., Mayeux P., Romeo P.H.,
RA  Giselbrecht S., Cartron J.P.;
RT  "Spleen focus-forming virus long terminal repeat insertional
RT  activation of the murine erythropoietin receptor gene in the T3c1-2
RT  friend leukemia cell line.";
RL  J. Biol. Chem. 266:6952-6956(1991).
RN  [6]

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RP  MUTAGENESIS.
RX  MEDLINE=93180826; PubMed=8382775;
RA  Miura O., Cleveland J.L., Ihle J.N.;
RT  "Inactivation of erythropoietin receptor function by point mutations
RT  in a region having homology with other cytokine receptors.";
RL  Mol. Cell. Biol. 13:1788-1795(1993).
CC  -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC  MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC  AND DIFFERENTIATION.
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC  -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC  -----
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CC  -----
DR  EMBL; J04843; AAA37571.1; -
DR  EMBL; X53081; CAA37248.1; -
DR  EMBL; M38133; AAA37572.1; -
DR  EMBL; M62360; AAA37582.1; -
DR  EMBL; S59388; AAB20029.2; -
DR  PIR; A32385; A32385.
DR  PIR; A41686; A41686.
DR  PIR; S13249; S13249.
DR  PIR; S14081; S14081.
DR  HSSP; P19235; 1EBA.
DR  MGD; MGI:95408; Epor.
DR  InterPro; IPR002996; CR1A.
DR  InterPro; IPR003961; FN-III.
DR  InterPro; IPR003528; Hematopo_receptor_L_F1.
DR  Pfam; PF00041; fn3; 1.
DR  SMART; SM00060; FN3; 1.
DR  PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW  Receptor; Transmembrane; Glycoprotein; Signal.
FT  SIGNAL 1 24
FT  CHAIN 25 507
FT  DOMAIN 25 249 ERYTHROPOIETIN RECEPTOR.
FT  TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).
FT  DOMAIN 273 507 POTENTIAL.
FT  DOMAIN 147 212 CYTOPLASMIC (POTENTIAL).
FT  DISULFD 52 62 FIBRONECTIN TYPE-III.
FT  DISULFD 90 106 BY SIMILARITY.
FT  CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CONFLICT 291 291 E -> D (IN REF. 3; AAB20029).
SQ  SEQUENCE 507 AA; 55194 MW; 067657A2E26451CA CRC64;

Query Match          67.7%; Score 869.5; DB 1; Length 507;
Best Local Similarity 77.7%; Pred. No. 3.4e-68;
Matches 164; Conservative 22; Mismatches 24; Indels 1; Gaps 1;

OY 1 KESKAAIIAARGPEELICFTEERLEDVCFEEAASAGVPGNFSFQLEDEPMKICRL 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 34 KESKAAIIAARGSEELICFTEERLEDVCFWEAASAGM-DNYSFSTQLEGSRSKSL 92
OY 61 HOAPTARCAIRPWCSLPTADTSSFPVLELRLTAASGAPRFHVIHINEVLLDAPVGLYA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 93 HOAPTVRGSRWPCSLPTADTSSFPVLELQVTEAASGSPRYHRIHINEVLLDAPAGLLA 152
OY 121 RIADSGHVIWMLPPETPMTSHIRFELDISAGNAGSVORVELLEGRTCVLSNLRG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 153 RAEEGSHVILWMLPPGAPMTTHIRYEDVSAAGNAGGTORVEVLEGRTCVLSNLRG 212
OY 181 TRITTAIVARMAEPSPFGFSAMSEPVSLT 211
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 213 TRYTFAVRARMAEPSPFGFSAMSEPVSLT 243

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RESULT 4
TPOR_MOUSE STANDARD; PRT; 625 AA.
ID TPOR_MOUSE STANDARD; PRT; 625 AA.
AC 008351;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia
DE protein) (C-mpl).
GN MPL OR TPOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX MEDLINE=93327753; PubMed=8334987;
RA Skoda R.C., Seidlin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,
RA Leder P.;
RT "Murine C-mpl: a member of the hematopoietic growth factor receptor
RT superfamily that transduces a proliferative signal.";
RL EMO J. 12:2645-2653(1993).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=ICFW; TISSUE=Petal liver;
RX MEDLINE=93309934; PubMed=8397366;
RA Vigon I., Florindo C., Fichelson S., Guenet J.-L., Mattei M.-G.,
RA Souvri M., Cosman D., Gisselbrecht S.;
RT "Characterization of the murine Mpl proto-oncogene, a member of the
RT hematopoietic cytokine receptor family: molecular cloning,
RT chromosomal location and evidence for a function in cell growth.";
RL Oncogene 8:2607-2615(1993).
CC -1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
CC -1- SIMILARITY: BELONGS TO THE CYOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL: Z22649; CA80365.1; -
DR EMBL: Z22657; CA80372.1; -
DR EMBL: X73677; CA52031.1; -
DR PIR: S3517; S3517.
DR HSSP: P19235; 1EBA.
DR MGD: MGI:97076; MPL.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003528; Hematopo_receptor_L_FL.
DR InterPro: IPR003561; FN_III.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_FL; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 25
FT CHAIN 26 625
FT DOMAIN 26 482
FT TRANSMEM 483 504
FT DOMAIN 505 625
FT CARBOHYD 117 117
FT CONFLICT 2 8
FT CONFLICT 99 99
FT CONFLICT 222 222
SQ SEQUENCE 625 AA; 69817 MW; 309CF6EAA3724549 CRC64;

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Query Match 13.3%; Score 171; DB 1; Length 625;
Best Local Similarity 24.6%; Pred. No. 2,4e-07;

```

Matches 62; Conservative 33; Mismatches 105; Indels 52; Gaps 8;
QY 4 SKAALLAARGPEELIFTERLEDLVCFEEASAGVPGNFSPQLEDEPMKLCRIHQ 63
QY 25 SQVFFLLALGTLEPDLNFCQFFEDLTCFMBEANA--PSGYQLLYAVRKPRACPLYSQ 82
QY 64 P7ARGAIREWCSLPTAD-TISSEVPLERLTAAS-GAPRRHVRHINEVLLDAPVGLVAR 121
QY 83 SVPTFGRRVYVCPADDEVLFPLHLWKNVSLNLTJLRYLFEVDSVGLPAPRYIKAR 142
QY 122 LADESGHYVIRW-LPPETPMTHIRELDI-----SAGNAGSVQVVELGRT----- 170
QY 143 GGSQPGELQTHWEAPAE--ISDFLHRELRYGPTDSSNATAPSV--TQLSTETCCPTLM 198
QY 171 -----ECVLSNLGRTRTITIAVRARMAEPPFG 197
QY 199 MRPNPVYLDPQPCVHPHAPSPHGPAPFLVYKGGSCLSVGLQAKSTWLDLRSPDGVSLR 258
QY 198 GFWSANSEPVSL 209
QY 259 GSWGPMSPFVTV 270
Db 198 GFWSANSEPVSL 209
Db 259 GSWGPMSPFVTV 270
RESULT 5
TPOR_HUMAN STANDARD; PRT; 635 AA.
ID TPOR_HUMAN STANDARD; PRT; 635 AA.
AC P40238;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia
DE protein) (C-mpl) (CD110 antigen).
GN MPL OR TPOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92302297; PubMed=1608974;
RA Vigon I., Morron J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
RA Gisselbrecht S., Souvri M.;
RT "Molecular cloning and characterization of MPL, the human homolog of
RT the v-mpl oncogene: identification of a member of the hematopoietic
RT growth factor receptor superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=94292186; PubMed=8020956;
RA Mignotte V., Vigon I., de Crevecoeur E., Romeo P.H., Lemarchandel V.,
RA Chretien S.;
RT "Structure and transcription of the human c-mpl gene (MPL).";
RL Genomics 20:5-12(1994).
CC -1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: C-MPL-K (SHOWN HERE) AND C-MPL-
CC P; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT A LOW LEVEL IN A LARGE NUMBER OF
CC CELLS OF HEMATOPOIETIC ORIGIN. THE TWO FORMS (C-MPL-K AND C-MPL-
CC P) ARE ALWAYS FOUND TO BE COEXPRESSED.
CC -1- DISEASE: DEFECTS IN MPL ARE A CAUSE OF CONGENITAL AMEGAKARYOCYTIC
CC THROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED BY ISOLATED
CC THROMBOCYTOPENIA AND MEGAKARYOCYTOPENIA WITH NO PHYSICAL
CC ANOMALIES.
CC -1- SIMILARITY: BELONGS TO THE CYOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-8 IS THE INITIATOR.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD10 entry;
CC WWW=http://www.ncbi.nlm.nih.gov/prow/guide/1158625.g.htm.
CC -----
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CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND SECRETED.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M84747; AAA58679.1; -
DR EMBL: S71404; AAB30844.2; ALT_SEQ.
DR EMBL: S71420; AAD14081.1; -
DR EMBL: L39064; AAC29513.1; -
DR PIR: B45268; B45268.
DR MIM: 300007; -
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 40
FT CHAIN 41 522 INTERLEUKIN-9 RECEPTOR.
FT DOMAIN 41 270 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 271 291 POTENTIAL.
FT DOMAIN 292 522 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 150 244 FIBRONECTIN TYPE-III.
FT DOMAIN 429 439 POLY-ASN.
FT DOMAIN 440 443 POLY-ASN.
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 331 331 R -> G (IN REF. 3).
FT CONFLICT 439 439 MISSING (IN REF. 3).
SQ SEQUENCE 522 AA; 57333 MW; E6CB5C6342DE2BB2 CRC64;

Query Match 8.9%; Score 114.5; DB 1; Length 522;
Best Local Similarity 22.1%; Pred. No. 0.016;
Matches 61; Conservative 32; Mismatches 110; Indels 73; Gaps 12;

QY 12 KGPPEE-LLCTFERLEDVCFEEAASAGVGPNGFSFQLEDEPMKLCRLHQAPTARGA 69
DB 47 QGPRSRFTCTLNINILIRICHM-SAPELQOG-----SSPWLFTSMQAPGSTRK 94
QY 70 IFMCSLPTADTSSFPVLELRLTAASG-APRFRHVIHINEV-----VLLDAP 115
DB 95 ----CILRSECTVVLPPPAVLVPSNDFTITFHCHMSGREQVSLVDPEYLPRRHVKLDPP 150
QY 116 VGLVARLADESGHVVIRW-LPPPEPMTSHIRFELDLSAGNGA-GSVQVELLEGRTGCV 173
DB 151 SFLQSNIS--SGHCILTWISIPALPEMTLLSYELAFKQOEAWBDAQIRHIVGTWLI 208
QY 174 LSNL-----RGRTRITIAVAR--MAEPSFGGFWASMSPEVS----- 208
DB 209 LEAFELDPGFIEHARLRLEMATLEDVVEEKRYTGOMSEDPVCPHAPROGRLPPWG 268
QY 209 -----LITGGGSRMEKLEOKYKELLRN 232
DB 269 WPGNTLVAVSIFLLLTGPLYLLFKLSPRVKRIEYON 304

RESULT 9
GHR_BOVIN
ID GHR_BOVIN STANDARD; PRT; 634 AA.
AC P79108;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
protein).
GN GHR.
OS Bos taurus (Bovine).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
CC Bovidae; Bovinae; Bos.
CC NCBI_TaxID=9913;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=GITR; TISSUE=liver;
CC Souza S.C., Wang X., Lobo R.B., Kopichek J.J.;
CC Submitted (Jul-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: X70041; CAA49635.1; -
DR HSSP: P10912; 1HMH.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 634 GROWTH HORMONE RECEPTOR.
FT DOMAIN 19 260 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 261 284 POTENTIAL.
FT DOMAIN 285 634 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 141 248 FIBRONECTIN TYPE-III.
FT DISULFID 56 66 BY SIMILARITY.
FT DISULFID 97 108 BY SIMILARITY.
FT DISULFID 122 136 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70979 MW; 91955A28296CB2E CRC64;

Query Match 8.8%; Score 112.5; DB 1; Length 634;
Best Local Similarity 26.3%; Pred. No. 0.029;
Matches 35; Conservative 25; Mismatches 60; Indels 13; Gaps 5;

QY 14 PELLCTFERLEDVCFEEAASAGV-GPGNFS-FSQLEDEPMKLCRLHQAPTARGAIR 71
DB 51 PKFTKCRSPLELTFSCWMTDGANHLSQSGVQMYIRIDIDEMKEC-----PDVVSAGE 105
QY 72 FMCSLPTADTSSFPVLELRLTAASGAPRFRHVIHINEVLLDAPGLVARLADES----- 126
DB 106 NSCYISSTYSVTWTPCYIKLITNSGIVD-HKCFSEVDIVQDPDPVGLMNTLINISLSTEIH 164
QY 127 GHVIVIRMLPPPEP 139
DB 165 ADILVKEPPPPPT 177

RESULT 10
GHR_SHEEP
ID GHR_SHEEP STANDARD; PRT; 634 AA.
AC Q28575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)


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DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
GN GHR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91099608; PubMed=1980117;
RA Adams T.E., Baker L., Fiddes R.J., Brandon M.R.;
RT "The sheep growth hormone receptor: molecular cloning and ontogeny of
RT mRNA expression in the liver."
RT Mol. Cell. Endocrinol. 73:135-145(1990).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL: M82912; AAA73171.1; -.
DR HSSP: P10912; IAX1.
DR InterPro: IPR002996; CRA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003528; Hematopo_receptor_L_FL.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_FL; 1.
DR Receptor: Transmembrane; Glycoprotein; Signal.
KW SIGNAL.
FT CHAIN 1 18
FT DOMAIN 19 634 GROWTH HORMONE RECEPTOR.
FT TRANSMEM 261 284 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 285 634 POTENTIAL.
FT DOMAIN 141 248 CYTOPLASMIC (POTENTIAL).
FT DISULFID 56 66 FIBRONECTIN TYPE-III.
FT DISULFID 97 108 BY SIMILARITY.
FT DISULFID 122 136 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70844 MW; FFD28B9C23EC1496 CRC64;

Query Match 8.6%; Score 110.5; DB 1; Length 634;
Best Local Similarity 26.6%; Pred. No. 0.044; Mismatches 57; Indels 13; Gaps 5;
Matches 34; Conservative 24;

19 CFTERLEDLVCFEEAASAGV-GPGNFS-PSFOLEDEPMKLCRLHQAPRTARGAIREWCSTL 76
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
56 CRSPLELEFSCWMTGDGNSHLSQSGSYQMYIRRDIGEWKEC-----PDVYSAGENCYF 110
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
77 PTADTSSFVPLELRLEAASAPRFRHYIHNEVLLDAPVGLVARLADES-----GHAVI 131
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
111 NSSYTSVWTFYCIKITSNGIIVD-HKCFSEVDIVQDPVGLMNTLINTSLTEIHADILV 169
: : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 132 RWLPPEPT 139
DB 170 KWPPPPPT 177

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RESULT 11
ID PRLR.CHICK
AC 004594; STANDARD; PRT; 831 AA.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (CPRLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
RT the cDNA sequence."
RT Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL: D13154; BAA02439.1; -.
DR PIR: J01655; J01655.
DR HSSP: P14787; IAN3.
DR InterPro: IPR002996; CRA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003528; Hematopo_receptor_L_FL.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01352; HEMATOPO_REC_L_FL; 1.
DR Receptor: Transmembrane; Glycoprotein; Signal; Repeat.
KW SIGNAL.
FT CHAIN 1 23
FT DOMAIN 24 831
FT TRANSMEM 439 459 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 460 831 POTENTIAL.
FT DOMAIN 25 122 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 1.
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 2.
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 3.
FT DOMAIN 36 46 FIBRONECTIN TYPE-III 4.
FT DISULFID 75 86 BY SIMILARITY.
FT DISULFID 59 59 BY SIMILARITY.
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94102 MW; 1CAE7591DCADBE9 CRC64;

Query Match 8.6%; Score 110; DB 1; Length 831;
Best Local Similarity 21.5%; Pred. No. 0.067;

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Matches 49; Conservative 39; Mismatches 94; Indels 46; Gaps 11.

OY 14 PEELCFETRLDVOCFEEASAGVPGNFSFQLEDEPMKLCRHOAPNARGAIRW 73
 DB 31 PFIIRCRSLKETFTSCGKPGSDGL-PNITLFTSKOSEE---ETPCPDRTSGPNS 85
 OY 74 CSLPDAUTSSFFVPLERLTA-----SGAPRHRVHINEVLLDAPVGLVARLADESG 127
 DB 86 CYENKHNHSPWTFNTVTATNEDISNSDPQ---VDTSIVQSPVNLLEFRSAN 142
 OY 128 --HVIIRMLPPETPTMTSH--IRFEL-----DISAGNAGSVORVELLEGRTTC 172
 DB 143 IMYLAKMSPPLADASSNHLHYELRIKPEKEEMETISVG-----VQ-----TQC 189
 OY 173 VLSNLRGRRTITAVRARAEPSPFGFMSANSEPVSLTGGGSRMEK 220
 DB 190 KINRLNAGMRVYVQVCTL-DP---GEWSEWSSERHILPSQSPPEK 233

RESULT 12
 GCN4_YEAST
 ID GCN4_YEAST STANDARD: PRT: 281 AA.
 AC P03069; P03069;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE General control protein GCN4 (Amino acid biosynthesis regulatory protein).
 GN GCN4 OR ANG9 OR AAS3 OR YEL009C.
 OS Saccharomycetes cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85038531; PubMed=6387704;
 RA Himebusch A.G.;
 RT "Evidence for translational regulation of the activator of general
 RT amino acid control in yeast."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6442-6446(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84298088; PubMed=6433345;
 RA Thireos G., Penn M.D., Greer H.;
 RT "5' untranslated sequences are required for the translational control
 RT of a yeast regulatory gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5096-5100(1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
 RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
 RA Chung E., Duncan M., Guzman E., Hartzell G., Hunkeler-Smith S.,
 RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
 RA Mosesdale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
 RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
 RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP DOMAIN.
 RX MEDLINE=87002456; PubMed=3530496;
 RA Hope I.A., Struhl K.;
 RT "Functional dissection of a eukaryotic transcriptional activator
 RT protein, GCN4 of Yeast."
 RL Cell 46:885-894(1986).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 250-281.
 RX MEDLINE=92054531; PubMed=1948029;
 RA O'Shea E.K., Klemm J.D., Kim P.S., Alber T.;
 RT "X-ray structure of the GCN4 leucine zipper, a two-stranded, parallel
 RT coiled coil."
 RL Science 254:539-544(1991).
 RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 226-281.
 RX MEDLINE=93113690; PubMed=1473154;
 RA Ellenberger T.E., Brandl C.J., Struhl K., Harrison S.C.;
 RT "The GCN4 basic region leucine zipper binds DNA as a dimer of
 RT uninterrupted alpha helices: crystal structure of the protein-DNA
 RT complex."
 RL Cell 71:1223-1237(1992).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 249-281.
 RX MEDLINE=99057965; PubMed=9837709;
 RA Eckert D.M., Malashkevich V.N., Kim P.S.;
 RT "Crystal structure of GCN4-pIQ1, a trimeric coiled coil with buried
 RT polar residues."
 RL J. Mol. Biol. 284:859-865(1998).
 RN [8]
 RP STRUCTURE BY NMR OF 237-281.
 RX MEDLINE=91367802; PubMed=1891459;
 RA Saudke V., Pastore A., Morelli M.A., Frank R., Gausepohl H.,
 RA Gibson T.;
 RT "The solution structure of a leucine-zipper motif peptide."
 RL Protein Eng. 4:519-529(1991).
 CC -I- FUNCTION: IS A TRANSCRIPTION FACTOR THAT IS RESPONSIBLE FOR THE
 CC ACTIVATION OF MORE THAN 30 GENES REQUIRED FOR AMINO ACID OR FOR
 CC PURINE BIOSYNTHESIS IN RESPONSE TO AMINO ACID OR PURINE
 CC STARVATION. BINDS AND RECOGNIZE THE DNA SEQUENCE:
 CC 5'-TGACGTCACA-3'.
 CC -I- SUBUNIT: BINDS DNA AS A DIMER.
 CC -I- SUBCELLULAR LOCATION: Nuclear.
 CC -I- SIMILARITY: BELONGS TO THE bZIP FAMILY. GCN4 SUBFAMILY.
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 CC -----
 DR EMBL: K02205; AAA34640.1; -;
 DR EMBL: K02649; AAA65521.1; -;
 DR EMBL: U18530; AAB64486.1; -;
 DR PIR: A03604; RGRYAL.
 DR PIR: A03605; RGRYAZ.
 DR PDB: 12TA; 15-APR-93.
 DR PDB: 22TA; 15-OCT-92.
 DR PDB: 1ISA; 31-OCT-93.
 DR PDB: 1DGC; 22-JUN-94.
 DR PDB: 1DGC; 08-MAR-96.
 DR PDB: 1GCL; 03-JUN-95.
 DR PDB: 1GCM; 29-JAN-96.
 DR PDB: 1SMI; 08-NOV-96.
 DR PDB: 12II; 07-JUL-97.
 DR PDB: 12IJ; 07-JUL-97.
 DR PDB: 12IK; 07-JUL-97.
 DR PDB: 12IL; 07-JUL-97.
 DR PDB: 12IM; 07-JUL-97.
 DR PDB: 1PIQ; 30-SEP-98.
 DR PDB: 1CE9; 25-MAR-99.
 DR TRANSFAC; T00321; -;
 DR SCD; S0000735; GCN4.
 DR InterPro; IPR001871; bZIP.
 DR Pfam; PF00170; bZIP; 1.
 DR SMART; SM00338; BRIZ; 1.
 DR PROSITE; PS00036; bZIP_BASIC; 1.
 KW Amino acid biosynthesis; Transcription regulation; Activator;
 KW DNA-binding; Nuclear protein; 3D-structure.
 FT DOMAIN 106 125
 FT DNA_BIND 231 249
 FT DOMAIN 253 274
 FT CONFLICT 239 281
 FT HELIX 227 276
 FT TURN 277 277
 ER -> PGVIVRESCKE (IN REF. 2).


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FT DOMAIN 17 237 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 238 261 POTENTIAL.
FT DOMAIN 262 608 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 117 223 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 72 83 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 608 AA; 68572 MW; D7IAD/B6C62528DC CRC64;

Query Match 8.3%; Score 107; DB 1; Length 608;
Best Local Similarity 26.7%; Pred. No. 0.084; Indels 32; Gaps 9;
Matches 54; Conservative 26; Mismatches 90;

OY 14 PELLCTERLEDLVCFEEAASAGVPGNFSFSQL-----EDEPKLCRLHQAPFANG 68
DB 29 PQISKCRSPLETFSCYWD-----GKVTSGTIGLLMKRSDDEMKEC-----PDYIT 77

OY 69 AIRFCSLPADTSSFPVLELRLTAASGAPRRHVIHNEVLLDAPVGLVARLADES-- 126
DB 78 AGENSCYFNTSYTSIMIPYCVKL-ANKDEVPEDEKCFSDVEIYLPDPVHLNLTNTLSQT 136

OY 127 ---GHAVIRMLDPPETPMTS---HIRELDISAGNGAGSVQVELLEGTECV--LSNR 178
DB 137 GIHGDIQVWMDPPPTADYQKGMITTELEYQYKEVNET---KWELEPLRSTVMPLYSLK 192

OY 179 GRTRTIIVARRM-AEPSFGF 199
DB 193 MGRDYEIRVRSRQRTSEKGEF 214

RESULT 15
GHR.COLLI STANDARD; PRT; 611 AA.
AC Q90375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).
GN GHR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=9932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.F.;
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
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DR EMBL: U20353; AAA84745.1; -
DR HSSP: P10912; IAYI
DR InterPro: IPR002896; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.

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DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 611 GROWTH HORMONE RECEPTOR.
FT DOMAIN 21 240 EXTRACELLULAR (POTENTIAL).
FT TRAMSEM 241 264 POTENTIAL.
FT DOMAIN 265 611 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 119 226 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT DISULFID 100 114 BY SIMILARITY.
FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 611 AA; 68851 MW; C48750BF9EE4BDA CRC64;

Query Match 8.1%; Score 104.5; DB 1; Length 611;
Best Local Similarity 26.2%; Pred. No. 0.14;
Matches 53; Conservative 28; Mismatches 96; Indels 25; Gaps 10;

OY 12 RGPPELLCTERLEDLVCFEEAASAGV-GPGNFSF-QLEDPEPKLCRLHQAPFANG 69
DB 27 RLPQISKCRSPLETFSCYWDGNGFNYSAPGTIGLLMKRDEDEMKEC-----PDYITA 81

OY 70 IRFWCSLPADTSSFPVLELRLTAASGAPRRHVIHNEVLLDAPVGLVARLADES-- 126
DB 82 GENSCYFNTSYTSIMIPYCVKLANKDEV--PDEKCFSDVEIYLPDPVHLNLTNTLSQT 139

OY 127 ---GHAVIRMLDPPETPMTS---HIRELDISAGNGAGSVQVELLEGTECV--LSNR 178
DB 140 GIHGDIQVWMDPPPTADYQKGMITTELEYQYKEVNET---KWELEPLRSTVMPLYSLK 195

OY 179 GRTRTIIVARRM-AEPSFGF 199
DB 196 IGRDYEIRVRSRQRTSEKGEF 217

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Search completed: August 28, 2002, 17:40:43
 Job time: 534 sec

